

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 17, 2001, 21:10:24 ; Search time 68.88 Seconds
(without alignments)
570,768 Million cell updates/sec

Title: US-09-456-306-2
Perfect score: 2885
Sequence: 1 MAHSYAEQLIDTLEACGVKR.....CGVGAMIDLARSINRINPTP 579

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1713	57.4	580	2	T34668 pyruvate dehydroge
2	1317.5	44.1	572	1	DEEPCPC pyruvate dehydroge
3	1101	36.9	572	2	D82984 pyruvate dehydroge
4	902.5	30.2	574	2	S01682 probable pyruvate
5	855	28.6	574	2	G69769 pyruvate oxidase h
6	744.5	24.9	590	2	C83382 probable decarboxy
7	637	21.3	553	2	D69162 pyruvate dehydroge
8	586.5	19.6	591	2	F64334 acetoacetate synth
9	576	19.3	577	2	C69059 acetoacetate synth
10	567	19.0	621	2	S75115 acetoaldehyde acid
11	554.5	18.6	574	2	B69644 acetoaldehyde synth
12	549	18.4	585	2	T11997 acetoaldehyde synth
13	546	18.3	612	2	A44857 acetoaldehyde synth
14	533.5	17.9	585	2	C70341 acetoaldehyde synth
15	533.5	17.9	590	1	S28920 acetoaldehyde synth
16	533.5	17.9	590	1	S73251 acetoaldehyde synth
17	526	17.6	618	2	F70855 probable llyb prot
18	523.5	17.5	562	1	YCEC1L acetoaldehyde synth
19	517.5	17.3	579	2	B44857 acetoaldehyde synth
20	515	17.3	548	1	YCEC1L acetoaldehyde synth
21	513	17.2	552	2	G69464 acetoaldehyde synth
22	508	17.0	613	2	T35828 acetoaldehyde synth
23	503	16.9	625	2	T45413 acetoaldehyde synth
24	502.5	16.8	584	2	B72362 acetoaldehyde synth
25	497	16.6	575	2	D69512 acetoaldehyde synth
26	493	16.5	670	1	YCMU acetoaldehyde synth
27	490.5	16.4	548	2	A82375 acetoaldehyde synth
28	490	16.4	548	2	D82634 acetoaldehyde synth
29	486	16.3	562	2	G75044 acetoaldehyde synth

30	482.5	16.2	681	2	T07968 acetoaldehyde synth
31	480	16.1	599	2	S15004 acetoaldehyde synth
32	480	16.1	555	2	S17691 acetoaldehyde synth
33	477	16.0	652	2	S29838 acetoaldehyde synth
34	464.5	15.6	621	2	JC5164 acetoaldehyde synth
35	461.5	15.5	681	2	T08085 acetoaldehyde synth
36	461	15.4	594	1	A56684 acetoaldehyde synth
37	461	15.4	626	1	A56684 acetoaldehyde synth
38	460	15.4	683	2	T07941 acetoaldehyde synth
39	457	15.3	683	2	T07912 acetoaldehyde synth
40	454	15.2	659	2	S60056 acetoaldehyde synth
41	454	15.2	664	1	YCNM2 acetoaldehyde synth
42	454	15.2	667	1	YCNM1 acetoaldehyde synth
43	451	15.1	638	2	S22490 acetoaldehyde synth
44	449	15.0	575	1	S35138 acetoaldehyde synth
45	447.5	15.0	601	2	I40666 acetoaldehyde synth

ALIGNMENTS

RESULT 1
T34668
pyruvate dehydrogenase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 31-Jan-2000
C:Accession: T34668
R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream,
submitted to the EMBL Data Library, December 1998
A:Reference number: Z21552
A:Accession: T34668
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-580 <SNU>
A:Cross-references: EMBL:AL034446; PIDN:CAA22389.1; GSPDB:GN00070; SCQEDB:SC1A9.19
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCQEDB:SC1A9.19
C:Superfamily: acetoaldehyde synthase large chain; thiamin pyrophosphate-binding domain

Query Match	Score	Length	DB 2;	Length	580;
Best Local Similarity	57.4%	57.5%	Pred. No. 1.7e-104;		
Matches 331;	Conservativity 92;	Mismatches 149;	Indels 4;	Gaps 4;	
QY	6	AEGLIDLEAGVKRITGLVGSLSNPVDAVRO-SDEWYVHVNNEEAAAFAGAESLITG	64		
DB	7	AEQFVDILTRAGVERLYGVGDSLPVDAVRRHSGIEVHVHRETAFAAGAEADITG	66		
QY	65	ELAVCAASCGPGNTNIIIOGLYDSHRNGAKVALASHPSAQISTPFOETHPELTPFEC	124		
DB	67	KLACAGSCGPGNHLINGLYDSHRNSAPVALASQIPSEIGLGFQETHPELTPFEC	126		
QY	125	GCEWVNGEGEGRILHAIQSTAGKSVVYIPGDIKEDAGDGTYSSTISGTPV	184		
DB	127	HYSELISPPKQMRLLQTAQAVGOGVSVSLPGDIAPRQGAETALVTS-RPTV	185		
QY	185	FDPPTFAALVEAINNAKSYTLFCGAGVKARQVLEAEKISPIGHALGQYIOHEN	244		
DB	186	RPDDEEDRLVRMIDADKTYLFCGSGTACGANAHEVMEFAKRLAPVONALRGKEFIQYDN	245		
QY	245	PRFVGGSLIGVACVDASNEADLLILGDPFYNAPLDPDVKAQIDVPRHGRSKL	303		
DB	246	PYVGGSGGLGYGANEATHECDLLILGDPFYNAPLDPDVKAQIDVPRHGRSKL	305		
QY	304	KYPVTGDAVTATINILPRHVEKTRDSFLDRMLKAHERKLSVVEYTHNNEKHYPIREY	363		
DB	306	DLAVMGDARETLRLIPRVEKKNRRLDMKKHADLGCVKAYTRKKDKNPIREY	365		
QY	364	VASILELADKDAVFYVDGTCMCVNHARYTENBGRDFGVGSRHGTMANLPHAIQAQ	423		
DB	366	VAALEMDADDVAVFYVDGTCMCVNHARYTENBGRDFGVGSRHGTMANLPHAIQAQ	424		

424 VDRNRVIAMCGDGLGMLLGLLTVKHLQPLKAVFNNSLGMVKLMLVEGQPEFGT 483
 425 TDRRQVVSMSGSGGFTLMGDELTLQHDLPVKIVLNNSSLGVELEMLVAGLPESHGV 484
 484 DHEEVFAELIAAAGIKSVRIIDPKKVRQDLAALAYPPGVLIDYTDNALSTIPPTTW 543
 485 ANKNPFAVAAEACGAFGVKVERKDLAGALAAFKHAKPALVDVTDNALSTIPKISA 544
 544 EOVMGFSKATRTVFGGVCAMIDLARSNIRNIPRP 579
 545 DMVTGALSRSKRLVDGGVGRMLQMARSLNRNRP 580
 RESULT 2
 DEPCPC
 pyruvate dehydrogenase (cytochrome) (EC 1.2.2.2) - Escherichia coli
 N.Alternate names: pyruvate oxidase
 C.Species: Escherichia coli
 C.Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 05-Nov-1999
 C.Accession: A23648; G64825; I55291; I57856
 R.Grabau, C.; Cronan Jr., J.E.
 Nucleic Acids Res. 14, 5449-5460, 1986
 A.Title: Nucleotide sequence and deduced amino acid sequence of Escherichia coli pyruvate
 A.Reference number: A23648; MUID:86286555
 A.Accession: A23648
 A.Molecule type: DNA
 A.Residues: 1-572 <GRA>
 A.Cross-references: GB:X04105; GB:M13947; GB:M13948; NID:9424272; PIDN:CAA27725.1; PID:94
 A.Experimental source: strain K-12
 R.Baltner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.Ross, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A.Title: The complete genome sequence of Escherichia coli K-12.
 A.Reference number: A64720; MUID:97426617
 A.Accession: G64825
 A.Status: nucleic acid sequence not shown; translation not shown
 A.Molecule type: DNA
 A.Residues: 1-572 <BLAV>
 A.Cross-references: GB:A8000188; GB:U00096; NID:91787084; PIDN:AAC73958.1; PID:g1787096;
 A.Experimental source: strain K-12, substrain MG1655
 R.Grabau, C.; Chang, Y.Y.; Cronan, J.E.
 J. Biol. Chem. 264, 12510-12519, 1989
 A.Title: Lipid binding by Escherichia coli pyruvate oxidase is disrupted by small altera
 A.Reference number: I55291; MUID:89308683
 A.Accession: I55291
 A.Status: translated from GB/EMBL/DBJ
 A.Molecule type: DNA
 A.Residues: 1-363, 'HE', 366-413, 'HGV', 417-572 <RES>
 A.Cross-references: GB:M28208; NID:g1009024; PIDN:AAB59101.1; PID:g1009025
 A.Experimental source: strain K-12
 R.Chang, Y.Y.; Wang, A.Y.; Cronan, J.E.
 Mol. Microbiol. 11, 1019-1028, 1994
 A.Title: Expression of Escherichia coli pyruvate oxidase (PoxB) depends on the sigma fac
 A.Reference number: I57856; MUID:94293772
 A.Accession: I57856
 A.Status: translated from GB/EMBL/DBJ
 A.Molecule type: DNA
 A.Residues: 1-22 <RE2>
 A.Cross-references: GB:S73268; NID:g685127; PIDN:AAB31180.1; PID:g685128
 C.Comment: The sequence of this protein was shown to be homologous with those of the lar
 ough pyruvate is the end product.
 C.Comment: This protein is not to be confused with a similar enzyme, pyruvate (or pyruv)
 ion of pyruvate to acetyl phosphate, carbon dioxide, and hydrogen peroxide.
 C.Genetics:
 A:Gene: poxB
 A:Map position: 19 min
 C:Complex: homotetramer
 C.Function:
 A:Description: catalyzes the conversion of pyruvate to acetate and carbon dioxide in the
 A:Note: in the presence of pyruvate and cofactor thiamine pyrophosphate, the addition of
 C:Specificity: acetylacate synthase large chain: thiamin pyrophosphate-binding domain
 C:Keywords: PBD; flavoprotein; homotetramer; lipid binding; magnesium; membrane protein
 F:422-470/Domain: thiamin pyrophosphate-binding domain homology <TPB>

F:50/Active site: Glu #status predicted

Query Match 44.1%; Score 1317.5; DB 1; Length 572;
 Best Local Similarity 46.3%; Pred. No. 1.3e-78;
 Matches 266; Conservative 106; Mismatches 195; Indels 7; Gaps 6;

1 MAHSAEOLIDTLEAGVKRIYGLYSDSLNPIYDVAV-RQSDIEWHVYNEEAFAAAAE 59
 1 MCOTAAATIAKTLESAGVKRIWGTGDSLNGSLNRMGTTEMTSTHEEVAFAAAAE 60
 60 SLITGELAVCAACGPGNTLITGLYDSHRGAKVLAIAHPSAIGSTFPOETHPRTL 119
 61 AQLSELAVCAACGPGNTLITGLYDSHRGAKVLAIAHPSAIGSTFPOETHPRTL 120
 120 FRECGCYEMVNGGQGERILHIAIQTSMAGKSVVVPIDIAKEDAGDGTYSNSTISS 179
 121 FRECHYCELVSPBOIVLAIAARKAVLNKGVSVVLPDVALKPAPEGA-TMHWYHA 179
 180 GTPVVEPPTAAALVEAIAINNAKSVTLFCGAGVKARAOVLELEKIKSPIGHALGKQY 239
 180 POPVTPPEEBELKLAQLRYSNIALMGSGGACAGHKELEFAGKIKAPIVHALRKEH 239
 240 IOHENPFEVNGSGLLGYACVADASNEADLLITLGTDFPYSPFLPKD-NVAQVDNGAHIG 298
 240 VEYDNPVYDGMTGLIGFSSGFHTMMNADTLVLLGTQFPYRAFYPDAKIIIDINPASIG 299
 299 RRTYKIVYTGDAVATINILPHYKEKTRDSFLDMKLAHERKLSVVEYTHNVEKHVP 358
 300 AHSKVDMAVLDISTLALLPLVEEKADRFELDKALEDY-RDARKGIDDLAKPSEK--A 356
 359 IHPEVVASILNEADKDAVFTVDGMCNWHARYIENDEGRDPSGRHGTMANALPHA 418
 357 IHPQIAQIISHFAADDAIFCDVGTPTVWAKRLK-MNGRRLLGSGNHOSMANAPQA 415
 419 TGAQSVDRNRVIAMCGDGLGMLLGLLTVKHLQPLKAVFNNSLGMVKLMLVEGQ 478
 416 LGAQTEBERQVAMCGDGGFSGMLMGDELTVQKPLKIVFNNSVLGFAFMAMKAGGY 475
 479 PEFGDHEEVFAELIAAAGIKSVRIIDPKKVRQDLAALAYPPGVLIDYTDNALSTIP 538
 476 LTWDGELHDIVFARIAECCITIGIRVERKASEVDALDRAESIDPVLVDVVAKEELAI 535
 539 PTTWEGMGFSKATRTVFGGVCAMIDLARSN 572
 536 PQLKEQAKGSLYMLAIRIISGRDEVIELAKTN 569

RESULT 3
 D82984
 pyruvate dehydrogenase (cytochrome) PA5297 [imported] - Pseudomonas aeruginosa (strain
 C:Species: Pseudomonas aeruginosa
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Sep-2000
 C:Accession: D82984
 R.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
 Nature 406, 959-964, 2000
 A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
 A:Reference number: A82950
 A:Accession: D82984
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-572 <STO>
 A.Cross-references: GB:AE004942; GB:AE004091; NID:g9951607; PIDN:AA080682.1; GSPDB:GN
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: poxB; PA5297

Query Match 36.9%; Score 1101; DB 2; Length 572;
 Best Local Similarity 40.6%; Pred. No. 1.9e-64;
 Matches 226; Conservative 116; Mismatches 208; Indels 6; Gaps 4;


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OY 354 EKHNP1HPEYVASILINLEADKDAVFTVDTGCMNWHARYENBEGTRDEYGSFRHCTMAN 413
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 403 R---PIRQYITVILNRELDLDAITITLDVGENGMWGFGRNQ-MKSTRGFSFOYTWGSMGF 458
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 414 ALPHAIQASQSDRRKOYIAMCGDGLMIGELLTVKVLHQLPKAVYFNNSISLGMKLEH 473
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 459 GLPAAIAQLAEFPDPROVCI-----NRRNLAMIQEQ 490
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 474 LVGEQPEGTDEHEENFAEIIAAGISVSRITDPKKKREQDLAEALAPGCVLIDITYDP 532
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 491 RVEGPPVQATLODCCDFGFAMENCGCGGLARVDEPELEDSVREALGTDGVGLVDITDE 549
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT

F64334
 acetylactate synthase (EC 4.1.3.18) large subunit - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C:Accession: F64334
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 R.; Reich, C.I.; Overbeek, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 R.; Bult, C.J.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kalne, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
 A.:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MUID:9637999
 A:Accession: F64334
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-591 <BU6>
 A:Cross-references: GB:U67483; GB:L77117; NID:g2826270; PIDN:AA898265.1; PID:g1591003; T
 C:Genetics:
 A:Map position: REV264626-262851
 C:Superfamily: acetylactate synthase large chain; thiamin pyrophosphate-binding domain
 C:Keywords: carbon-carbon lyase; oxo-acid-lyase
 F:436-464/Domain: thiamin pyrophosphate-binding domain homology <TP>

[illegible]

```

Db      412  SFLASGGLGTGPGFGRPAIGAKVAKPRANVTISTITGGDFLMSNELATISBYDIPVVICI 471
Oy      461  FNNSSLGWV-KLEMLVSGQPEFTGD-HBEVFEAIAAAGIKSVRTDPPKVRQLEAL 518
Db      472  FDNRLTGVWYQMNLYYGQROSEVHLSESPDFVKLAESYGVKADRIISPDIEKKLEAI 531
Oy      519  AYPGPVLIDIVTDP-NAL-STTP 539
Db      532  LSNPEYLLDIDVDPALPMP 554

```

RESULT 9

C69059
acetoacetate synthase (EC 4.1.3.18) large chain - Methanobacterium thermoautotrophicum
C:Species: Methanobacterium thermoautotrophicum
C:Date: 03-Dec-1997 #sequence_rev:10n 03-Dec-1997 #text_change 15-Oct-1999
C:Accession: C69059
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.
; Qiu, D.; Spadafora, R.; Vitale, R.; Wang, Y.; Wierzbowski, J.; Gibson, J.; Jilwan,
K., S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A>Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta
H
A:Reference number: A69000; MUID:98037514
A:Accession: C69059
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-577 <MTH>
A:Cross-references: GB:E000666; NID:92622541; PID:AMB85919.1; PID:g2622556
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH444
A:Start codon: GTG
C:Superfamily: acetoacetate synthase large chain; thiamin pyrophosphate-binding domain
;Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein
;4428-476/domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match	19.3%	Score 576	DB 2	Length 577
Best Local Similarity	26.8%	Pred. No. 4.2e-30		
Matches 149	Conservative 117	Mismatches 267	Indels 24	Gaps
OY	7	EQLDITLEAGCKRYTGLVGDLSLNPIYDAVRSODLEWVNRNEEAAPAGAESLITGL	66	
DB	8	QALISLSDGQADYVFGPGGQLRLPYDLMLYSEKLIHLVREQCAAHAAADYARASGV	67	
OY	67	AWCAASGPGNHLTLOGLYDSHRNCAKVALYASHIPSAGISGTFPOETHPEILFKECSCY	126	
DB	68	GVCITFSGPGAINLVLTGATATAMDSPAPIYALAGOVPTHLIGDAOEYDMIGITMPITKH	127	
OY	127	CEWVNGEKGGERILHHAIOSTWAGK-GVSVVYPDDIAKEDAGDGTYSNSTISSGTPVVF	185	
DB	128	SFQPSDASEIRPIYVASEFHIAKTGPRGPVYIDLPIDQEOIME-EVDDLELPGRPNVK	186	
OY	166	PDPTBAALVLEAINNAKSTYLLFCAGV--KNRAQVYLEAEIKSPIGALGCKOYIOME	243	
DB	187	GHPIDIKRAELIRSEKRVYIAGGCVITISGASREIKELSDIKAPVTTTTLGKKSFPED	246	
OY	244	NFEFVMSGLLGAGCAVDASNEADLLILGTFP-----YSDFLPKDVAVQDINGAII	297	
DB	247	HPSANGMLGMHGRKKAANLVYDECDCLINAGCFSDRTTCNVAFAPMARIIHVYDIPALI	306	
OY	298	GRRITVYKPYTGDAVATLENILPNVK--EKYDRSFLDRMLKAHERKLSSVETVYHNVEK	355	
DB	307	GKNVGVDPPIVGDADANNVIRELIATLKKYEKRDSOMLESYQK-----ADCMRPMASYD	359	
OY	356	HVPIHREVVASLITNEDLADKDAVFYTDGSCNVMHARYIENPGSTRDVFSGFRHGMANML	415	
DB	360	EYPLRPQOVIKETSIVLDEYVITVDGONQMMMAHFTTS-RAPRKFTISSGGLGTMGCFE	418	
OY	416	PHAIAGQSDVRNRQYIANGCGDGLMLGELLTVLHQLPLKAVVFNNSSIGMVLKLEMLY	475	
DB	419	PAIAGAKVALPDSDVAVVACGGGFLMVGODLATIIEYDIPVIGICIMDRNHLGMAVQMQRL	478	

QY 476 EGOPEFGTTH--EEVNFADIAAAGIKSVRTDPKKVRQLEALAYGSPVLIDIVTDPN 533
DB 479 FYDERMSHHLGVDPFVLAESFVEAREIEEPGETSALRSRATGSPALDIYDIPD 538
QY 534 AL--SIPPTITWEQVWG 548
DB 539 EILPMVPPCGGLEITVG 555

RESULT 10
S75115
acetylcholine synthase - *Synechocystis* sp. (strain PCC 6803)

N:Alternate names: protein sir2088
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S75115
R:Kaneke, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimp, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M. Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
A:Reference number: S74322; MUID:97061201
A:Accession: S75115
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-621 <KAN>
A:Cross-references: EMBL:D90910; GB:AB001339; NID:g1652956; PIDN:BAA17977.1; PID:g165306
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Gene: *llvG*
A:Start codon: GTG
C:Superfamily: acetylcholine synthase large chain; thiamin pyrophosphate-binding domain

Query Match 19.0%; Score 567; DB 2; Length 621;
Best Local Similarity 27.4%; Pred. No. 1.8e-29;
Matches 164; Conservative 113; Mismatches 236; Indels 86; Gaps 18;

QY 9 LIDTLEAGVKKRIYGLVDSLNPIYDAVQ---SDIEVHVRNEEAAFAAGESLITG 64
DB 27 LMDSLKRGVKKHIFPGCALPIYDELRYFAAGEIHLVLRHNGSHADGAKRATG 86
QY 65 ELAVCAASGCGPNTLHIOGLYDSHRNGAKVLAISHIPSAIGSTPFOE-----THPEI 118
DB 87 KVGVEGSGCGPNTLHIOGLYDSHRNGAKVLAISHIPSAIGSTPFOE-----THPEI 146
QY 119 LKESGSGCEWNGGEGEERILHNAIOSTMAGK-GVSVVVIRPGDIKE-----DADGG 170
DB 147 -----KSHYVRSADMARITETAFHILASTGRPEVILIDIPKDVGLDECEYIPLDPGD- 199
QY 171 TYSNSTISSGTPVPPDETEAAALVEAINNAKSVTLFCGAG--VKNARQVLELAETIKS 228
DB 200 ---VNLPGYRPTVKGPNQINAAQLLEQARNPLLYGGGAIANNAHQVEFAERQQL 255
QY 229 PIGHALGKQYIQHNPPEVGMSCILGYACVDASNEADLILIGTDF-----PYSDFL 282
DB 236 PVTTLIMIGAFDENHPSVGMIGMGTAVANFVSECDLILAVGARPDRTVGTGLDEFA 315
QY 283 PKDVAQVDINGAHIGRTYKVPYTGVAATIENTILPHVKE-----KIDRSIDLMFL 335
DB 316 SRAKVIHIDIDAEYGNKRAPDVPYGVRYVRLQLQRARELLDPTPHPTTQALNR-- 373
QY 336 KAHREKLSSVVEYTHANEKVPRIHPEYVA--SILNELADK--DAVFTVDTGMCVNHAR 391
DB 374 -----IDHMKTDYPLQVPHEDTIAQOEYVHETIGRARPAYITTDVGQOMMAAQ 423
QY 392 YIENPEGTRDVGSRGTANALPHATGAOSVDNRNOVIAMCGDGLIGMLIGLITVYL 451
DB 424 FLNN--GFRRWISSAGLTGFGFLAAMGAKVGVGDEAVICISDASFOYMLQELGTLAQ 481
QY 452 HQDLKAVNFVNSLSGMK-----LEMLVSGQPEFGIDHEVNAETIAAAAGT 499

DB 482 YDIQVKTIIINMGWGNVROMOQTFEERYSAKNSQGM-----DINL--LCEAYGI 532
QY 500 KSVRTDPKKVRQLEALAYGSPVLIDIV--DPNAL-SIPPTITWEQVWGSPKAAT 555
DB 533 KGIYRKREDLAPATAEMLAHNGPVMVYVKKDENCYPMIAPGMSNOMLGEPEVVR 591

RESULT 11
B69644

acetylcholine synthase (EC 4.1.3.18) large chain - *Bacillus subtilis*

C:Species: *Bacillus subtilis*
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: B69644; 139865
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabis, C.; Ferrari, Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallazzi, A.; Lech, J.; Harwood, C.R.; Henault, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Koecker, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Liao, Y. M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portele, Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scand, A:Authors: Schleich, S.; Schroeter, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Se, akouchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A:Authors: Yoshikawa, H.F.; Zunshtein, E.; Yoshikawa, H.; Dancho, K.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*
A:Reference number: B69580; MUID:98044033
A:Accession: B69644
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-574 <KUN>
A:Cross-references: GB:299118; GB:AL009126; NID:g2635200; PIDN:CAB14791.1; PID:g26352
A:Experimental source: strain 168
R:Grandoni, J.A.; Zahler, S.A.; Galvo, J.M.
J. Bacteriol. 174, 3212-3219, 1992
A:Title: transcriptional regulation of the *llv-leu* operon of *Bacillus subtilis*.
A:Reference number: 139865; MUID:92250415
A:Accession: 139865
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-20, 'R' <RES>
A:Cross-references: GB:M87009; NID:g143096; PIDN:AAA22550.1; PID:g143097
C:Genetics:
A:Gene: *llvB*
C:Superfamily: acetylcholine synthase large chain; thiamin pyrophosphate-binding
C:Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein
F:443-491/Domain: thiamin pyrophosphate-binding domain homology <rpB>
F:64/Active site: Glu #status predicted

Query Match 18.6%; Score 554.5; DB 2; Length 574;
Best Local Similarity 28.7%; Pred. No. 1.1e-28;
Matches 154; Conservative 113; Mismatches 251; Indels 19; Gaps 9;

QY 4 SYAQLIDTLEAGVKKRIYGLVDSLNPIYDAVQSDIEVHVRNEEAAFAAGESLIT 63
DB 19 SGALMLIESLKEKEVEMIFPGGAVPIYDKLYNSGLVILHRHNEGALHAAEGVARVS 78
QY 64 ELAVCAASGCGPNTLHIOGLYDSHRNGAKVLAISHIPSAIGSTPFOEITHPEIIFKEC 123
DB 79 GKPGVATISGPGATNLVTLGADAMISDPLVYFTGVAVNSVGSADFQADLIGTIMPV 138
QY 124 SGCEWNGGEGEERILHNAIOSTMAGK-GVSVVVIRPGDIKEDAGDGTYSNSTISSG-T 181
DB 139 TKHSYQVROPEDDPRITKEAFHIAATGRPGVILIDIPKDVATIE-GRFSYDHENMLPGYQ 197
QY 182 PVVPPDTEAAALVEAINNAKSVTLFCGAGVKNARA--QVLELAETIKSPIGHALGKQY 239
DB 198 PTEPNYLOLRKLEAVNAKKPVYILAGAGVHLGKASEELKNVNEQOQITVAVHTLLGLG 257
QY 240 IOHENPFEVGMSCILGYACVDASNEADLILIGTDF-----YSDFLPKDVAQVDIN 293

Db 258 FRADHPLFGMAGMCHGTYTANMALHCDLLISTGARDDREVTLKHFARNMAIAHLDID 317
OY 294 GAHIGRTTYKVPVTDGVAATENILPHVEKRTDRSFLDMLKAHERKLSVETHTNV 353
Db 318 PAETGIMKTQIPVVDSDKIVLOELKODKOSDSEMKKOLEMKEEYPL--WVVDNE 374
OY 354 EKHVPIHPEYVASILNELADKDAVFTVDTGMCVNHARYTENEGTRDFEVGSFRHGTMAN 413
Db 375 EE--GFKPOKLEYIHQFTKGALVATDVGOHQMSAQFPFGKADK--WYSSGGLTGMF 431
OY 414 ALPHAIQAQSVDRNRQVIAMCGDGLMLGELLTYKHLQPLKAVVFNNSLGMVK--L 471
Db 432 GLPAAIGAOIAEKDAIVAVAVAGDGFOMTLOEILDVIREMLPVKVVILNACLGWVROMQ 491
OY 472 EMLVEGQPEFGTDEHVEVFAEIAAGIKSVRTDTPKKEVREOLAEPGLVID 528
Db 492 ELPYERYSKSPASQDPVKLSAEYAIKIRISSEAEKLEALTSREPVVIDV 548

RESULT 12

T11997
acetylhydroxyacid synthase large subunit - red alga (Cyanidium caldarium) chloroplast
C:Species: Chloroplast Cyanidium caldarium
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-May-2000
C:Accession: T11997
R:Gloeckner, G.; Rosenthal, A.; Valentín, K.
submitted to the EMBL Data Library, September 1997
A:Description: Organization of 46 kb of the Cyanidium caldarium Rkl plastid genome.
A:Reference number: Z17374
A:Accession: T11997
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-585 <GLO>
A:Cross-references: EMBL:AF022186; NID:92465730; PIDN:AAB82660.1; PID:92465731
A:Experimental source: strain Rkl
C:Genetics:
A:Genome: chloroplast
A:Note: 11VB
C:Superfamily: acetylactate synthase large chain; thiamin pyrophosphate-binding domain
C:Keywords: chloroplast
P:446-494/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 18.4%; Score 549; DB 2; Length 585;
Best Local Similarity 27.3%; Pred. No. 2.5e-28;

Matches 160; Conservative 112; Mismatches 247; Indels 68; Gaps 15;

OY 9 LIDTLEAGCVKRIYGLVGSLSNPIDVAV---RQSDIEWVHVRNEEAFAAGAESLITG 64
Db 16 LIDMLVKIHKVNIIFGPGAILPIYDELYHMEKKLIKIHVLRHESAAHAAVAVRATN 75
OY 65 ELAVCAASGCGPNTILIOGLYDSHRNGAKVLAISHIPSAQISTGTFQETHPRELFKES 124
Db 76 EGVGVCLATGCPGATNLVTGATRAQMDSPRIATIGOVSRFAITGTDFAFOEIDIGITPLTY 135
OY 125 GCEVNGEAGEGRILNHAIQSTMAK--GVSVVYIPGDIAKEDAG----DGTSSNSTISS 179
Db 136 KHSFVRDRDSDISTYSEAFYISKHGRPGAVLIDPKDGLGEEFNHVDSDIDHPRTIK 195
OY 180 GTPVVPDPTEAALVEAALINNAKSVTLFCGAGVKNARAQ--VLELAEKIKSPIGHALGK 237
Db 196 YRTIYGRPJOIEKFKMLLESKOPILYVGAGVMSRAHGEIEELASFIKIPVTTLMGK 255
OY 238 QYIQHNEPFEVHSGGLGACVDASNEADLLILGTDG-----PYSDFLPDQNAQVD 291
Db 256 GSFENEYNPYLGLMGHNGTAAYANFAVSECDLLIALGAREPDRVYTGKLDSEACNAQYIHVD 315
OY 292 INGAUIGRRTYKVPVTDGVAATENILPHVKEKTDTSFLDRMLKHAHERKLSVETHTNV 351
Db 316 IDPAETGKRRITQALIIISDIKIVLEKLSMKEGTNN--MDK-----NOTQAMLDH 363
OY 352 NVEK-----HVP-----IHPEYVASILNELADKDAVFTVDTGMCVNHARYTENEGT 399

Db 364 RIHKWKVEYPLSIPHDSKILLYPOEVINEISQIAOK-AFATVDVGQHOHMAAOELKVBQG- 421
OY 400 RDEVGSRHCTMNAALPHAIQAQSVDRNRQVIAMCGGGGLMLGELLTYKHLQPLKAV 459
Db 422 -KWLSSGSLTGMVGLPAAIGAKIANPNDLITICTGASFOMLQELGTIAOVELDIKIF 480
OY 460 VFNNSSLGMVKL-----EMLVEGQPEFGTDEHVEVFAEIAAGIKSVRTDP 507
Db 481 IINNQGAVYROMQOAFYDQRYAHSMNAKQPD-----FVQLANSIGIKIRYTT 531
OY 508 KKVREOLAELAYPGVLLD--IVTDPNAL-SIPPTTWQVNGFSK 551
Db 532 KDLKSRTIERITSPGPIIDICVATSENCYPMIAPGKSNQSMGLTK 578

RESULT 13

A44857
acetylactate synthase (EC 4.1.3.18) - Spirulina platensis
C:Species: Spirulina platensis
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 15-Oct-1999
C:Accession: A44857
R:Milano, A.; De Rossl, E.; Zanaria, E.; Barbierato, L.; Clifert, O.; Riccardi
J. Gen. Microbiol. 138, 1399-1408, 1992
A:Title: Molecular characterization of the genes encoding acetylhydroxy acid synthase
A:Reference number: A44857; WUID:92381487
A:Accession: A44857
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-612 <MIL>
A:Note: sequence extracted from NCBI backbone (NCBI:112275, NCBI:112276)
C:Superfamily: acetylactate synthase large chain; thiamin pyrophosphate-binding domain
C:Keywords: branched-chain amino acid biosynthesis; carbon carbon lyase; oxo-acid-lyase
P:446-494/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 18.3%; Score 546; DB 2; Length 612;
Best Local Similarity 26.6%; Pred. No. 4.2e-28;

Matches 164; Conservative 123; Mismatches 253; Indels 76; Gaps 19;

OY 6 AEDLITLEAGCVKRIYGLVGSLSNPIDVAV---AVRQSDIEWVHVRNEEAFAAGAESL 61
Db 15 AFRILDSLKRNGVQHIFGPGAILPIYDELYRAEAEGDIOHILVRHOGASHAADGYAR 74
OY 62 INGEVLVCAASGCGPNTILIOGLYDSHRNGAKVLAISHIPSAQISTGTFQET----- 114
Db 75 ATGRVGVCEGTSGPGATNLVTGATRAQMDSPRIATIGOVSRFAITGTDFAFOEIDIGITL 134
OY 115 ---HPEILFEKESGCEVNGEAGE--RILNHAIOSTMAK--GVSVVYIPGDIKED- 166
Db 135 PIYKHSYV-----REPGDMATIVAEAHIASTGPRPVLLIDVPRDVGLEEF 181
OY 167 ---AGDGYVSNSTISSGTPVVPDPTEAALVEAALINNAKSVTLFCGAGV--KNARAQVL 220
Db 182 DYIPVNPGEVS--LRGVRPTVKGAVRQIQAIIKEABRPLMYVGGAISATPAHMEA 238
OY 221 ELAEKIKSPIGHALGKQYIQHNEPFEVHSGGLGACVDASNEADLLILGTDG----- 276
Db 239 ELAEILOPIVTTLMKGSEFDEKHPLSVGLMGHNGTAAYANFAVSECDLLIALGAREPDRV 298
OY 277 --PYSDFLPDQNAQVDINGANIGRRTYKVPVTDGVAATENILPHVKEKTD----- 327
Db 299 TGLDDEFGSAKAYIHIDIPAEVGNKRTPEVPIYGVROYLHILRRCRFTIGVGNQNT 358
OY 328 RSEFLDRMLKAHERKLSVETHTNVNEKHVPIHPEYVASILNELADKDAVFTVDTGMCNV 387
Db 359 OSWLEIRINRPE--DYPLVVPYSDS-----LAPQVYIABLGA--PDGYVTTDVQGNOM 410
OY 388 WHARTYENPEGTDYFVSGFRHGTMANALPHAIQAQSVDRNRQVIAMCGDGLMLGELL 447
Db 411 WAOQFLKN--GPRQWISAGLGTMGYGIPSMGAKVALERSQVICTIAGDASVQMNIOELG 468
OY 448 TVKLHQLPLKAVVFNNSSLGMVKLEMLVEGQPEFGTDEHVEV--NPAETIAAAGIKSVRI 504

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Job time: 2596 sec

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